

FIGURE 1

1
 ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCTGGAG
 MetAlaProLeuAlaGluValGlyGlyPheLeuGlyGlyLeuGlu
 46
 GGCTTGGGCCAGCAGGTGGGTTCGCATTTCTGTTCCTCCTGCC
 GlyLeuGlyGlnGlnValGlySerHisPheLeuLeuProProAla
 91
 GGGGAGCGGCCCGCTGCTGGGCGAGCGCAGGAGCGCGCGGAG
 GlyGluArgProProLeuLeuGlyGluArgArgSerAlaAlaGlu
 136
 CGGAGCGCGCGCGGGCGGGGGCTGCGCAGCTGGCGCACCTG
 ArgSerAlaArgGlyGlyProGlyAlaAlaGlnLeuAlaHisLeu
 181
 CACGGCATCTGCGCCGCCGCGCAGCTCTATTGCCGCACCGGCTTC
 HisGlyIleLeuArgArgArgGlnLeuTyrCysArgThrGlyPhe
 226
 CACCTGCAGATCCTGCCCGACGGCAGCGTGCAGGGCACCCGGCAG
 HisLeuGlnIleLeuProAspGlySerValGlnGlyThrArgGln
 271
 GACCACAGCCTCTTCGGTATCTTGAATTCATCAGTGTGGCAGTG
 AspHisSerLeuPheGlyIleLeuGluPheIleSerValAlaVal
 316
 GGAATGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGA
 GlyLeuValSerIleArgGlyValAspSerGlyLeuTyrLeuGly
 361
 ATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCC
 MetAsnAspLysGlyGluLeuTyrGlySerGluLysLeuThrSer
 406
 GAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACC
 GluCysIlePheArgGluGlnPheGluGluAsnTrpTyrAsnThr
 451
 TATTCATCTAACATATATAAACATGGAGACACTGGCCGCAGGTAT
 TyrSerSerAsnIleTyrLysHisGlyAspThrGlyArgArgTyr
 496
 TTTGTGGCACTTAACAAAGACGGAAGTCCAAGAGATGGCGCCAGG
 PheValAlaLeuAsnLysAspGlyThrProArgAspGlyAlaArg
 541
 TCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCACTG
 SerLysArgHisGlnLysPheThrHisPheLeuProArgProVal
 586
 GATCCAGAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTAC
 AspProGluArgValProGluLeuTyrLysAspLeuLeuMetTyr
 631
 ACT
 Thr

Query: 170 TGGCGCACCTGCACGGCATCCTGCGCCGCGGCAGCTCTATTGCCCGCACCGGCTTCCACC 229
Sbjct: 2 TGGATCATTTAAAGGGGATTCTCAGGCGGAGGCAGCTATACTGCAGGACTGGATTTCTACT 61

Query: 230 TGCAGATCCTGCCCCACGGCAGCGTGCAGGGCACC CGGCAGGACCACAGCCTCTTCCGTA 289
Sbjct: 62 TAGAAATCTTCCCCAATGGTACTATCCAGGGAACCAGGAAAGACCACAGCCGATTTGGCA 121

Query: 290 TCTTGGGAATTCATCAGTGTGGCAGTGGGACTGGTTCAGTATTAGAGGTGTGGACAGTGGTC 349
Sbjct: 122 TTCTGGAATTTATCAGTATAGCAGTGGGCCTGGTTCAGCATTTCAGGCGTGGACAGTGGAC 181

Query: 350 TCTATCTTGGGAATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCCGAAT 409
Sbjct: 182 TCTACCTCGGGATGAATGAGAAGGGGGAGCTGTATGGATCAGAAAACTAACCCAAGAGT 241

Query: 410 GCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACCTATTTCATCTAACATATATA 469
Sbjct: 242 GTGTATTTCAGAGAACAGTTTCGAAGAAAACTGGTATAATACGTACTCGTCAAACCTATATA 301

Query: 470 AACATGGAGACACTGGCCGCAGGTATTTTGTGGCACTTAACAAAGACGGAACCTCCAAGAG 529
Sbjct: 302 AGCACGTGGACACTGGAAGGCGATACTATGTTGCATTAAATAAAGATGGGACCCCGAGAG 361

Query: 530 ATGGCGCCAGGTCCAAGAGGCATCAGAAAATTTACACATTTCTTACCTAGACCAGTGGATC 589
Sbjct: 362 AAGGGACTAGGACTAAACGGCACCAGAAAATTCACACATTTTTTACCTAGACCAGTGGACC 421

Query: 590 CAGA 593
Sbjct: 422 CCGA 425

FIGURE 3

>gb:GenBank accession number -ID:AB020858|acc:AB020858 Homo sapiens genomic DNA of p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 1/11 - Homo sapiens, 100000 bp.

Minus Strand HSPs:

A.

Score = 1430 (214.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 288/289 (99%), Positives = 288/289 (99%),
Strand = Minus / Plus

```
Query: 289 TACCGAAGAGGCTGTGGTCTGCCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 230
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 15927 TACCGAAGAGGCTGTGGTCTGCCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 15986

Query: 229 GGTGGAAGCCGGTGC GGCAATAGAGCTGCCGGCGGCGCAGGATGCCGTGCAGGTGCGCCA 170
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 15987 GGTGGAAGCCGGTGC GGCAATAGAGCTGCCGGCG -CGCAGGATGCCGTGCAGGTGCGCCA 16045

Query: 169 GCTGCGCAGCCCCCGCCCCGCGCGCGCTCCGCTCCGCGCGCTCCTGCGCTCGCCCA 110
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 16046 GCTGCGCAGCCCCCGCCCCGCGCGCGCTCCGCTCCGCGCGCTCCTGCGCTCGCCCA 16105

Query: 109 GCAGCGGCGGCCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCACCTGCTGGCCCA 50
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 16106 GCAGCGGCGGCCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCACCTGCTGGCCCA 16165

Query: 49 AGCCCTCCAGGCCGCCAGAAAGCCCCGACTTCGGCTAAGGGAGCCAT 1
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 16166 AGCCCTCCAGGCCGCCAGAAAGCCCCGACTTCGGCTAAGGGAGCCAT 16214
```

B.

Score = 1224 (183.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 250/255 (98%), Positives = 250/255 (98%),
Strand = Minus / Plus

```
Query: 633 AGTGATACATCAGTAGGTCCTTGTACAATTCTGGAACCTTTTCTGGATCCACTGGTCTAGG 574
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7257 AGTGATACATCAGTAGGTCCTTGTACAATTCTGGAACCTTTTCTGGATCCACTGGTCTAGG 7316

Query: 573 TAAGAAATGTGTAAATTTCTGATGCCTCTTGGACCTGGCGCCATCTCTTGGAGTTCCGTC 514
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7317 TAAGAAATGTGTAAATTTCTGATGCCTCTTGGACCTGGCGCCATCTCTTGGAGTTCCGTC 7376

Query: 513 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 454
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7377 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 7436

Query: 453 ATAGGTGTTATACCAAGTTCTCTTCAAACCTGCTCCCTAAAGATGCATTGGAAGTAAGTTT 394
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7437 ATAGGTGTTATACCAAGTTCTCTTCAAACCTGCTCCCTAAAGATGCATTGGAAGTAAGTTT 7496
```

FIGURE 3 (cont.)

Query: 393 CTC-TGATCCATAGA 380
 ||| ||| | |||
 Sbjct: 7497 CTCCTGAAAGAGAGA 7511

C.

Score = 530 (79.5 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
 Identities = 106/106 (100%), Positives = 106/106 (100%),
 Strand = Minus / Plus

Query: 391 CTGATCCATAGAGTTCTCCTTTGTCATTTCATTCCAAGATAGAGACCACTGTCCACACCTC 332
 |||||
 Sbjct: 9837 CTGATCCATAGAGTTCTCCTTTGTCATTTCATTCCAAGATAGAGACCACTGTCCACACCTC 9896

Query: 331 TAATACTGACCAGTCCCACTGCCACACTGATGAATTCCAAGATACC 286
 |||||
 Sbjct: 9897 TAATACTGACCAGTCCCACTGCCACACTGATGAATTCCAAGATACC 9942

FIGURE 4

Sequences analyzed:

1. HUMAN FGF-9 (P31371_HUMAN FGF-9) [SEQ ID NO:9]
2. MOUSE FGF-9 (P54130_MOUSE FGF-9) [SEQ ID NO:10]
3. RAT FGF-9 (P36364_FGF9_RAT FGF-9) [SEQ ID NO:11]
4. XENOPUS XFGF-CX (BAA83474Xen; Xenopus laevis XFGF-CX) [SEQ ID NO:12]
5. FGF-CX (cgAB020858) [SEQ ID NO:2]

Multiple Alignment:

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGF-CX

FGF-CX

```

M A P L G E V G N Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L N D H L G Q S E A G G L P R G P A V T D L D H
M A P L A D V G T F L G G Y D A L G - Q V G S H F L L P P A K D S P L L F N D P L A Q S E R L S R - S L A P - - S D L S H
M A P L A E V G G F L G G L G L G Q Q V G S H F L L P P A G E R P P L L G E R R S A A E R S A R - G G P G A A Q L A H

```

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGF-CX

FGF-CX

```

L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L Q G I L R R R Q L Y C R T G F H L Q I L P D G N V Q G T R Q D H S R F G I L E F I S V A T G L V S I R G V D S G L Y L
L H G I L R R R Q L Y C R T G F H L Q I L P D G S V Q G T R Q D H S L F G I L E F I S V A V G L V S I R G V D S G L Y L

```

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGF-CX

FGF-CX

```

G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N D K G E L Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S N L Y K H G D S G R R Y F V A L N K D G T P R D G T
G M N D K G E L Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S N L Y K H G D T G R R Y F V A L N K D G T P R D G A

```

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGF-CX

FGF-CX

```

R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R A K R H Q K F T H F L P R P V D P E K V P E L Y K D L M G Y S
R S K R H Q K F T H F L P R P V D P E R V P E L Y K D L L M Y T

```

FIGURE 5

FGF-CX	MAPLAEVGGFL EGLEGLQGVESHFLPPA GERFPILLGERSAERSAR - EGP GAAQLAH	59
XFGF-2U	MAPLADVGTFL EGYDALG - QVESHFLPPAKDSFLLFNDDPLAQSERLSE - SAP - - SDSLH	56
FGF-9	MAPLGEVGNMFEVQDAVP - - FENVPVL P - - VDSFVLLSDHLGQSEAGGLPRPPAVTEL DH	56
FGF-16	- - - MAEVGGVFASLDWDLHGFS SLGNVPLADSPGFLNERLGLIEGKLQRES P - - TDFAH	55
FGF-CX	LHGILRRRLYCRTGTFHLQILPDDGSWQGTRODHSLEFGILEFISVAVGLVSIRGVDSCGLYL	119
XFGF-20	LQGIILRRRLYCRTGTFHLQILPDDGNWQGTRODHSRFGILEFISVALGLVSIRGVDSCGLYL	116
FGF-9	LKGILRRRLYCRTGTFHLEIFPENGITQQGTRKDHRSRFGILEFISLAVGLVSIRGVDSCGLYL	116
FGF-16	LKGILRRRLYCRTGTFHLEIFPENGITVHGTRHDHSRFGILEFISLAVGLLSIRGVDSCGLYL	115
FGF-CX	GMNDKGELYGSEKLTSECI FREQFEENWYNTYSSNLYKHGDTGRRYFVALNKDGTPRDGA	179
XFGF-20	GMNDKGELYGSEKLTSECI FREQFEENWYNTYSSNLYKHGDSGRRYFVALNKDGTPRDGT	176
FGF-9	GMNEKGELYGSEKLTQECV FREQFEENWYNTYSSNLYKHVDTGRRYFVALNKDGTPREGT	176
FGF-16	GMNERGELYGSKKLTRECV FREQFEENWYNTYASTLYKHSDSERQWYVVALNKDGSPREGY	175
FGF-CX	RSKRHQKFTTHFLPRP VDPERVPPELYKDL LMYT	211
XFGF-2U	RAKRHQKFTTHFLPRP VDPEKVPPELYKDL LMGYS	208
FGF-9	RTKRHQKFTTHFLPRP VDPDKVPPELYKDL LLSQS	208
FGF-16	RTKRHQKFTTHFLPRP VDPSKLPMSRDL FHR	207

FIGURE 6

ptnr:SWISSPROT-ACC:P31371 GLIA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST GROWTH FACTOR-9) (FGF-9) (HBGF-9) - HOMO SAPIENS (HUMAN), 208 aa. Identities = 147/208 (70%), Positives = 170/208 (81%)

Query:	1	MAPLA	EVGGFLGGLG	QQVGS	HFLLPP	AGERPP	LLGERR	SA	AERS	ARG-GPGAAQLAH	59
Sbjct:	1	MAPL	GEVGN	YFGVQDAV	--PFGNV	PLPV--DSPV	LLSDHL	GQSEAGGLPRGPAV	TDLDH	56	
Query:	60	LHGIL	RRRQLY	CR	TGFHLQ	ILPD	GSVQ	GT	QDHS	LF	GI
Sbjct:	57	LKGI	LR	RRQLY	CR	TGFHL	E	IFP	NGT	IQ	TR
Query:	120	GMNDK	GELYG	SEKLT	SECI	FREQ	FEEN	WYNTY	SSNIY	KHGD	TGRRYF
Sbjct:	117	GMNEK	GELYG	SEKLT	QECV	FREQ	FEEN	WYNTY	SSNLY	KHVD	TGRRY
Query:	180	RSKR	HQKFT	HL	PR	VP	DP	PERV	PELY	KD	LL
Sbjct:	177	RTKR	HQKFT	HL	PR	VP	DP	DP	KV	PELY	KD

FIGURE 7

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

Query:

1 MAPLAEVGGFLGGLGQQVGSFLLPPAGERPPLLGERSSAAERSARG-GPGAAQLAH 59
||||| + | + + | + || + || + ||

Sbjct:

1 MAPLGEVGSYFGVQDAV--PFGNVPLPV--DSPVLNDHLCQSEAGGLPRGPATVDLDH 56

Query: 60 LHGILRRRLQYCRGTGFHLQLIPLDGSVQGTRQDHSLFGILEFISVAAGLVSIRGVDSGLYL 119
| | | | | | | | | | | | | | + | | | | | | | | | | | |
Sbjct: 57 LKGIILRRRLQYCRGTGFHLEIFPNNGTIOGTRKDHSRFGILEFISIAVG LVSIRGVDSGLYL 116

[illegible]

Query: 180 RSKRHQKFTFLPRPVDPERVPELYKDIL 208
| + | | | | | | | | | | | | | | | + |
Sbjct: 177 RTKRHQKFTFLPRPVDPKVPPELYKDIL 205

FIGURE 8

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
 Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

Query:	1	MAPLA	EVGGFLG	GLEGLG	QQVGS	HFLLPP	AGERP	PLLGERR	SAARS	ARG-GPG	AAQLAH	59
				+		+	+		+		+	
Sbjct:	1	MAPLGE	VGSYFG	VQDAV	--PFG	NVPLPV	--DSP	VLLSDH	LQSEAG	GLPRGP	AVTDLDH	56
Query:	60	LHGIL	RRRQLY	CR	TGFHLQ	ILPD	GSVQ	TRQD	HS	LF	GILEFIS	119
Sbjct:	57	LKGIL	RRRQLY	CR	TGFHLQ	ILPD	GSVQ	TRQD	HS	LF	GILEFIS	116
Query:	120	GMNDK	GELYG	SEKLT	SECIF	REQF	EENW	NTYSS	NIYKH	GDTGR	RYFVAL	179
Sbjct:	117	GMNEK	GELYG	SEKLT	QECV	FREQ	FEEW	NTYSS	NLYKH	VDTGR	RYFVAL	176
Query:	180	RSKR	HQKFT	HF	LP	RP	VD	PER	VP	ELY	KDLL	208
Sbjct:	177	RTKR	HQKFT	HF	LP	RP	VD	PD	KV	PELY	KDIL	205

FIGURE 9

FGF-CX Query Length = 211
XFGF-CX Sbjct Length = 208

Plus Strand HSPs:

Score = 906 (318.9 bits), Expect = 4.4e-90, P = 4.4e-90
Identities = 170/211 (80%), Positives = 189/211 (89%), Frame = +1

Query:	1	MAPLAEVGGFLGGLGQQVGS	60
		+ +	
Sbjct:	1	MAPLADVGTFLGGYDALGQ-VGSHFLLPPAKDSPILLFNDPLAQSERLSRSAP--SDL	57
Query:	61	HGILRRRLYCRGTGFHLQILPDG	120
		+ +	
Sbjct:	58	QGILRRRLYCRGTGFHLQILPDG	117
Query:	121	MNDKGELYGSEKLTSECIFREQ	180
		+ +	
Sbjct:	118	MNDKGELYGSEKLTSECIFREQ	177
Query:	181	SKRHQKFTHTFLPRPVDPERVPELYKD	211
		+ + +	
Sbjct:	178	AKRHQKFTHTFLPRPVDPEKVP	208

FIGURE 10

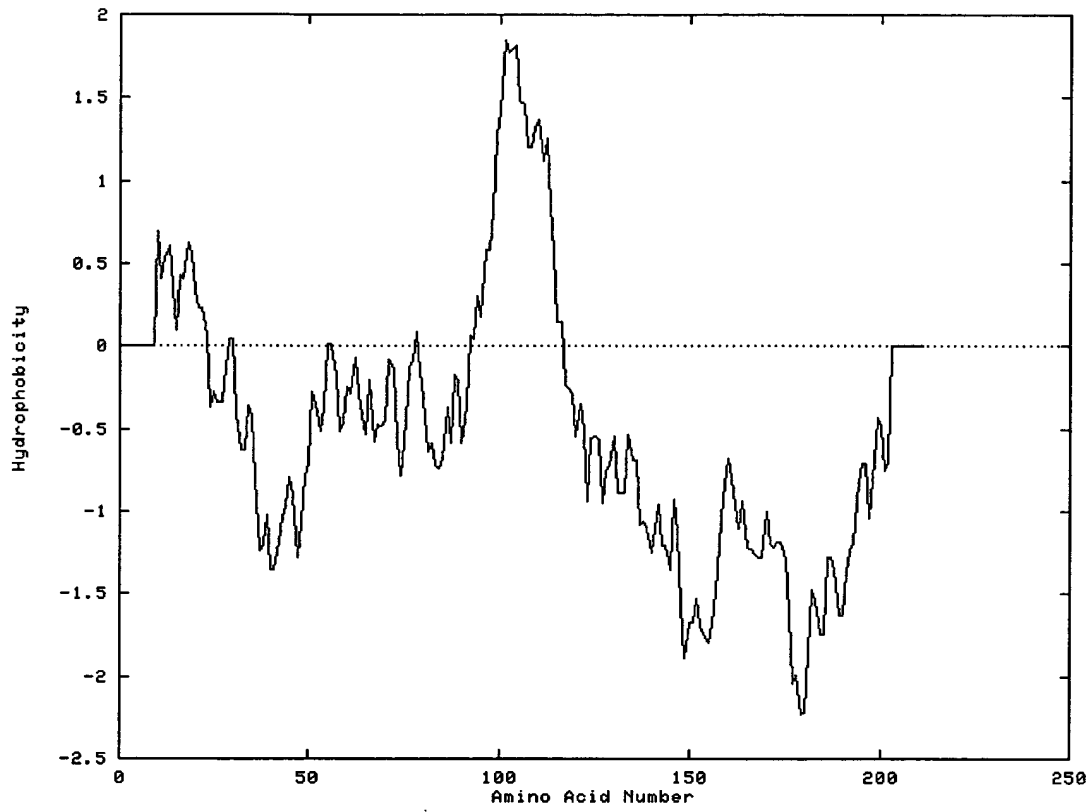
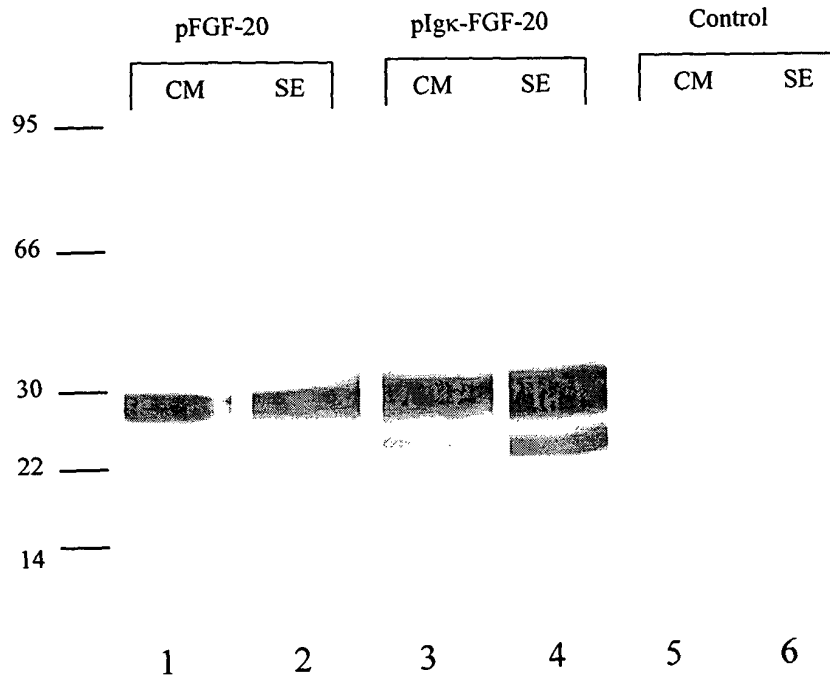


FIGURE 11

Panel A



Panel B

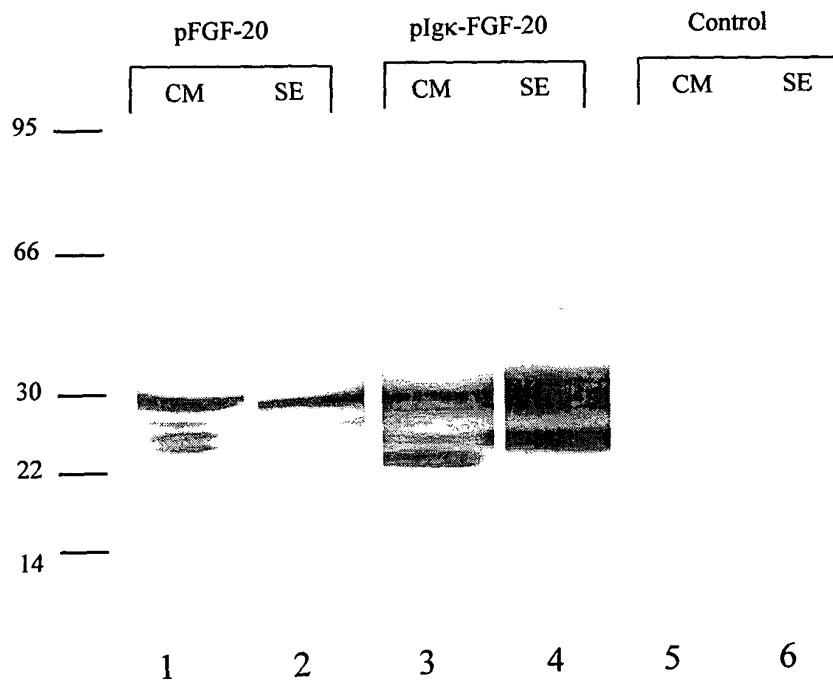


FIGURE 12.

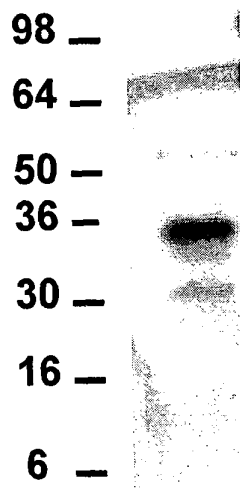


Figure 13.

Exon 1
 ...AGACAGTGAGAGCTTCCCTGCCATTTCAGTGTCAAAGTCCCTCCGGAGCGACCTCAGAGGAGTAACCGGGCCCTTAAC
 TTTTGGGCTCGTTTGTCTATAAATTTTCTCTATCCACCTCCATCCACCCCAACACTCTTTACTGGGGGGTCTTTT
 GTGTTCCGGATCTCCCTCCATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGCGGGCTTGAGGGCTTGGGCCAGCA
 1 M A P L A E V G G F L G G L E G L G Q Q
 GGTGGTTGCGATTTCCTGTGCTCCTGCCGGGAGCGCGCGCTGTGGCGAGCGCAGGAGCGCGGAGCGGA
 21 V G S H F L L P P A G E R P P L L G E R R S A A E R S
 GCGCGCGGGCGGGGCTGCGCAGCTGGCGCACCTGCACGGCATCTCGCGCGCGGCGAGCTCTATTGCCGCACC
 48 A R G G P G A A Q L A H L H G I L R R R Q L Y C R T
 GGCTTCCACCTGCAGATCCTGCCCGACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTATCTTGGAAAT
 74 G F H L Q I L P D G S V Q G T R Q D H S L F G I L E F
 CATCAGTGTGGCAGTGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGGAAATGAATGACAAGGAGAAC
 101 I S V A V G L V S I R G V D S G L Y L G M N D K G E L
 TCTATGGATCAGAGAACTTACTTCCGAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACCTATTCATCT
 128 Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S
 AACATATATAACATGGAGACACTGGCCCGCAGGTATTTTGTGGCACTTAACAAAGACCGAACTCCAAGAGATGGCGCCAG
 154 N I Y K H G D T G R R Y F V A L N K D G T P R D G A R
 GTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCAGAAAGAGTTCCAGAATTGTACAAGGACC
 181 S K R H Q K F T H F L P R P V D P E R V P E L Y K D L
 TACTGATGTACACTTGA...
 208 L M Y T

<-|-> Exon 2

<-|-> Exon 3

Figure 14.

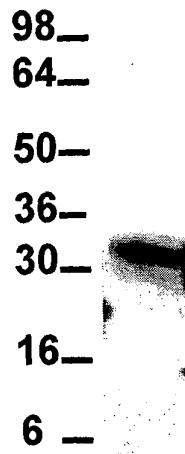


Figure 15, Panel A.

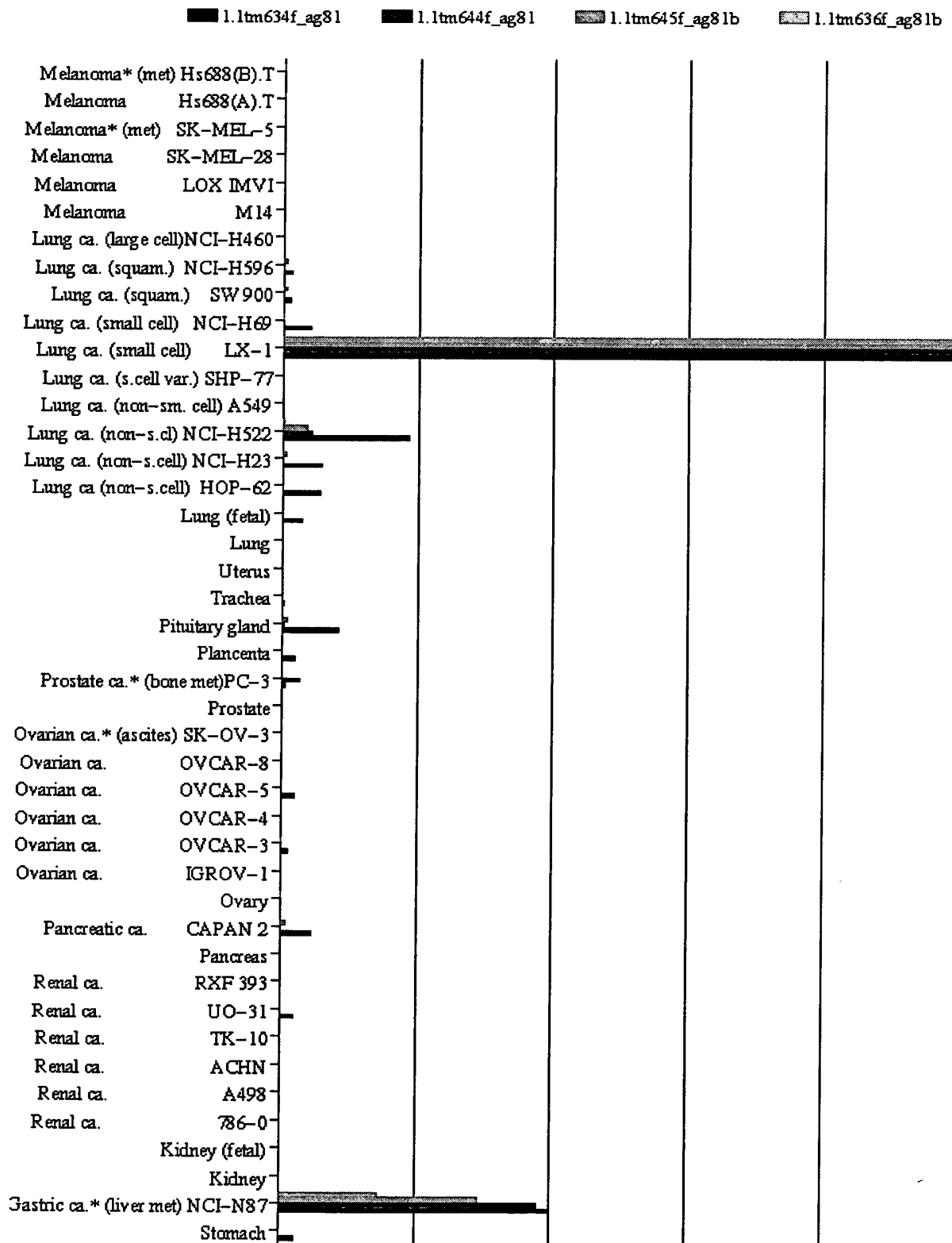


Figure 15, Panel B.

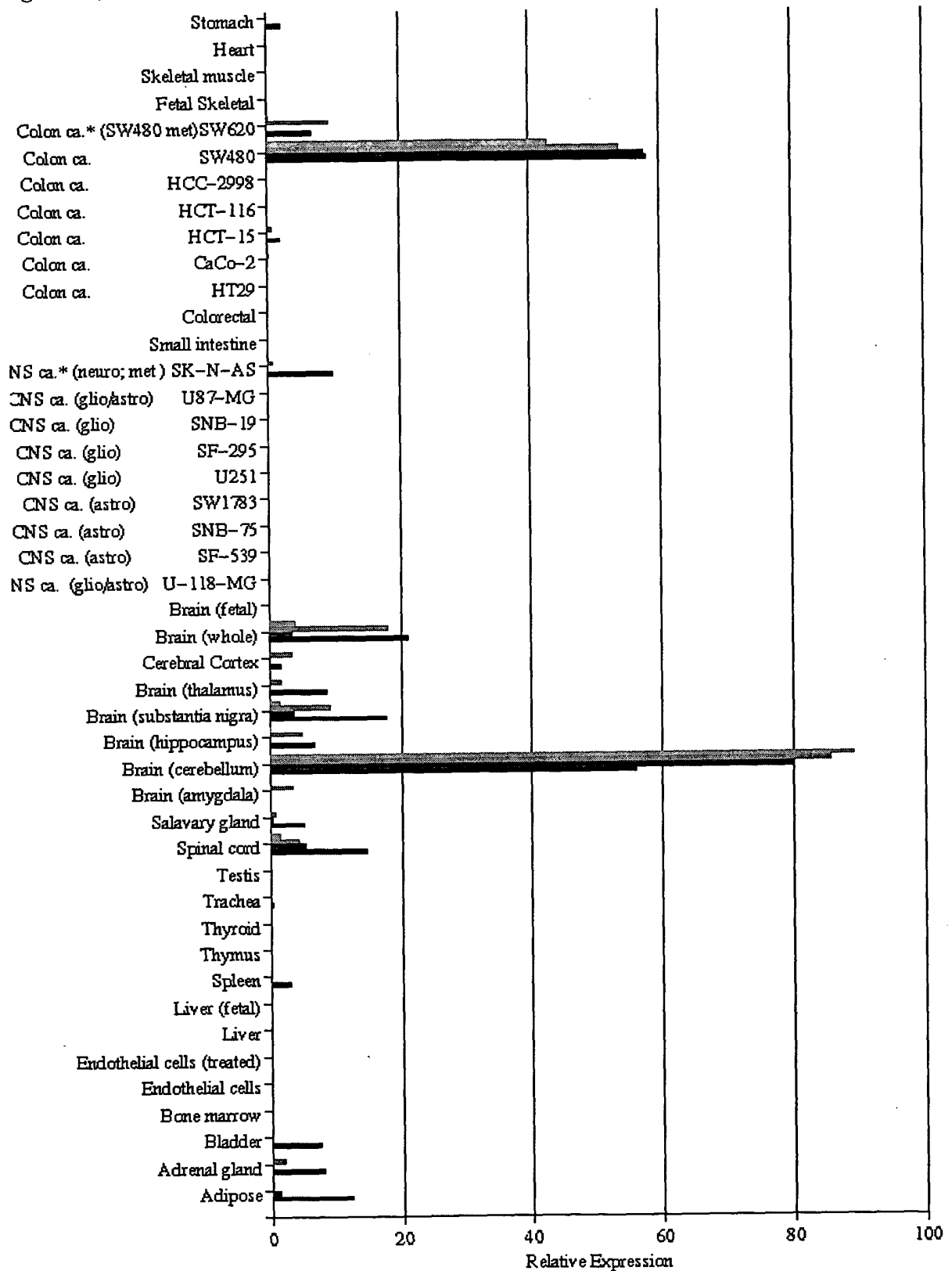


Figure 15, Panel C.

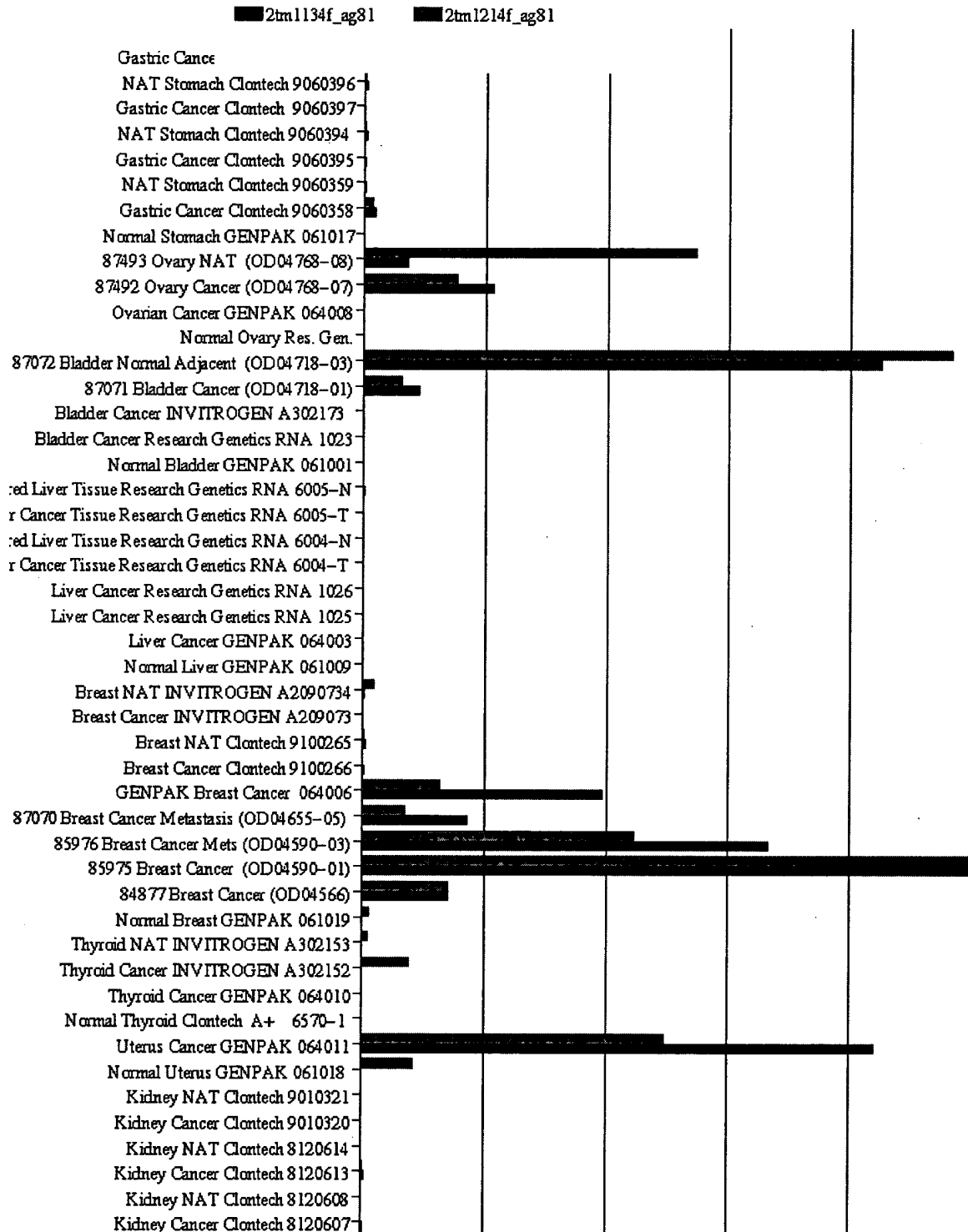


Figure 15, Panel D.

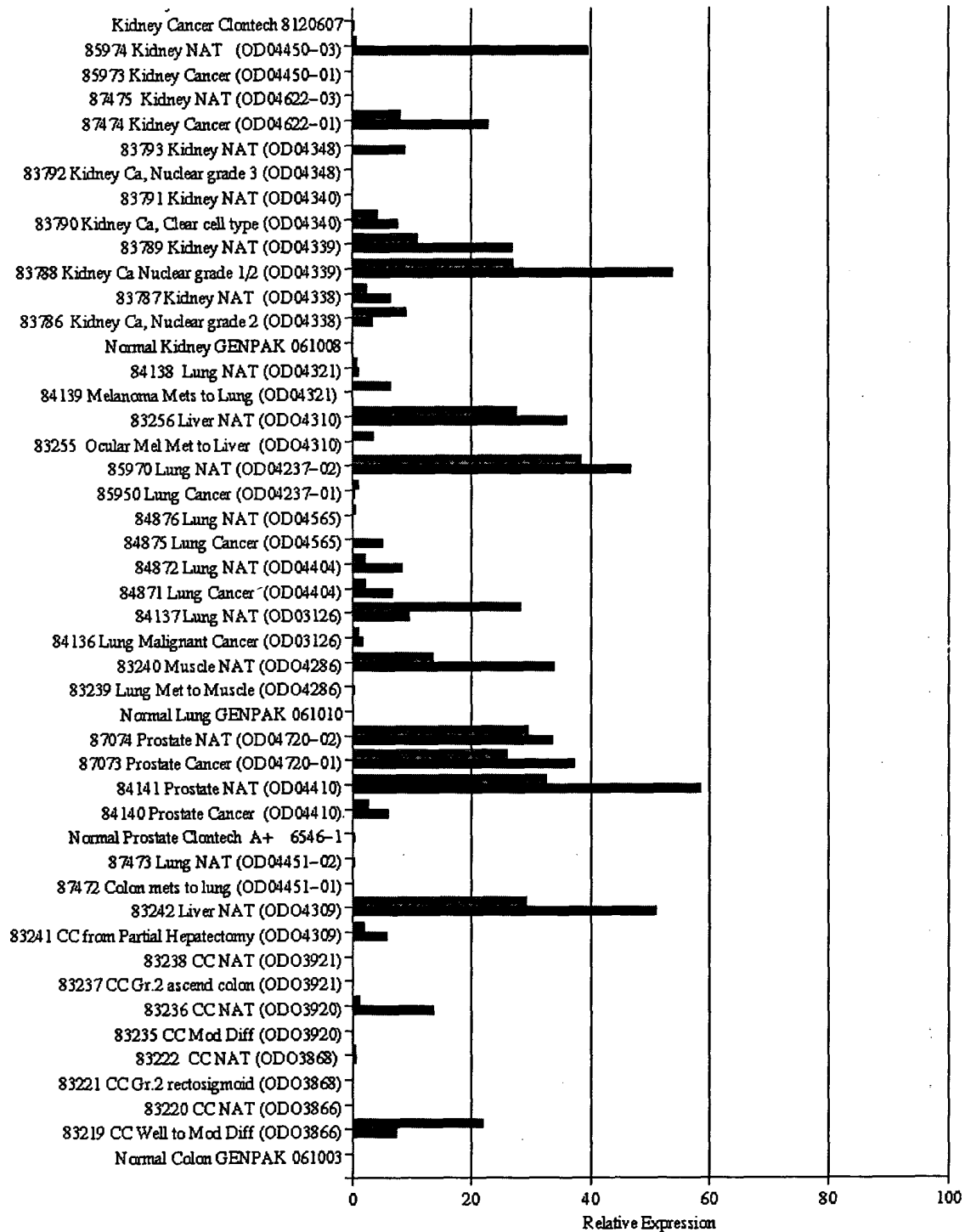


FIGURE 16.

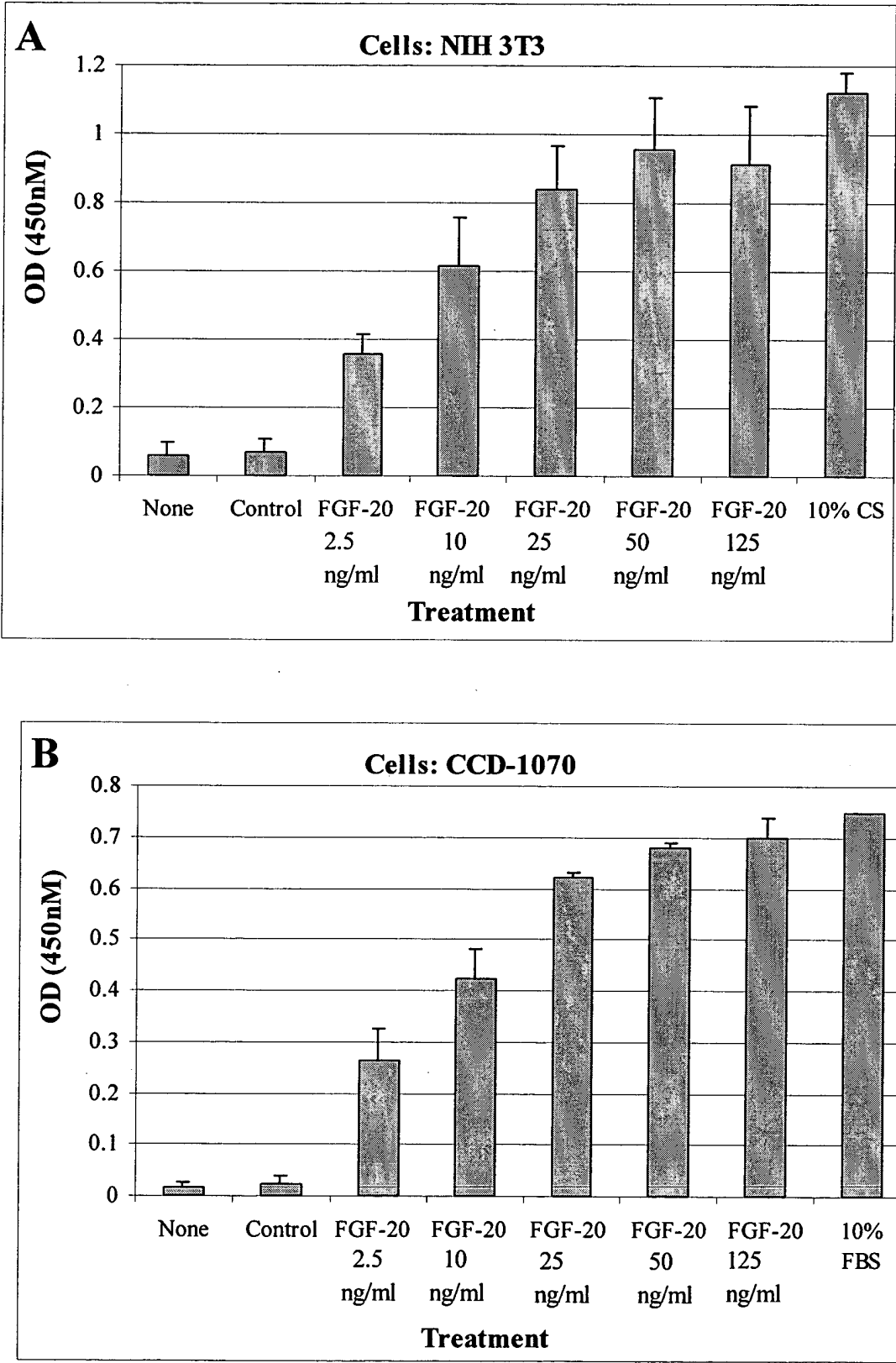


FIGURE 16 (continued).

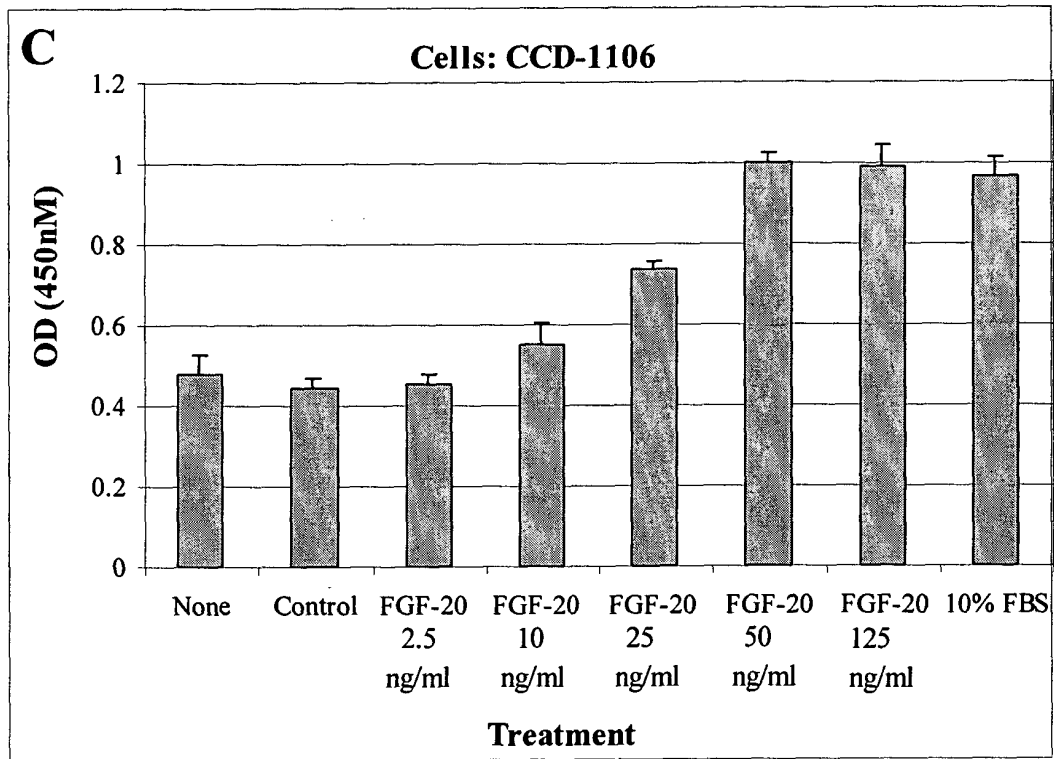


FIGURE 17.

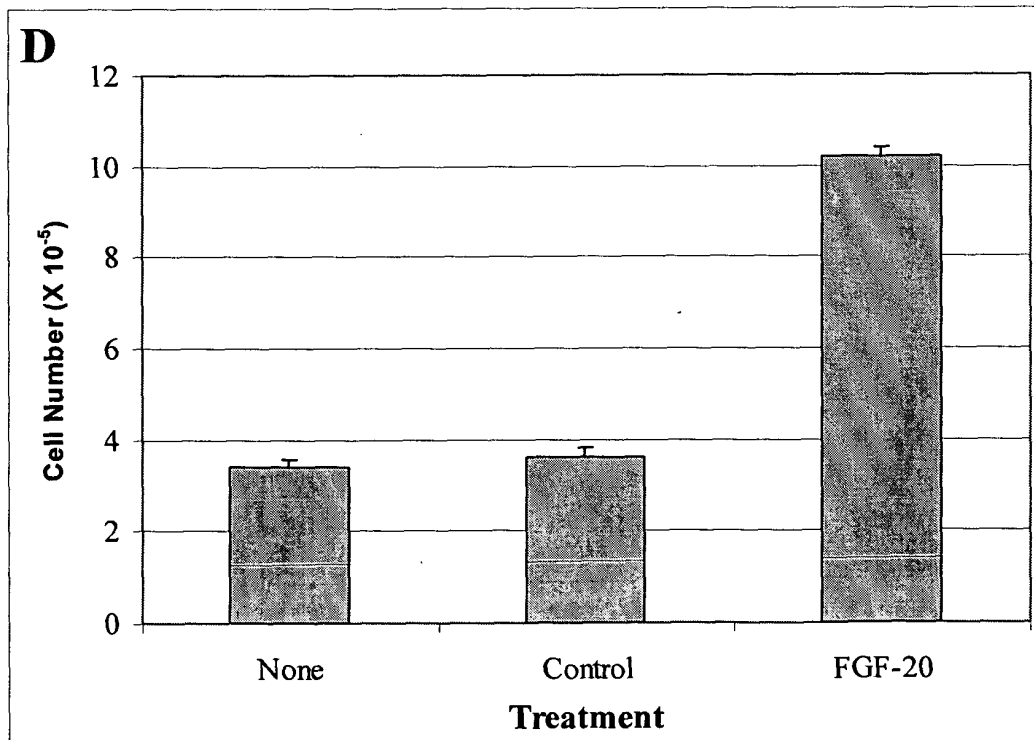


FIGURE 18.

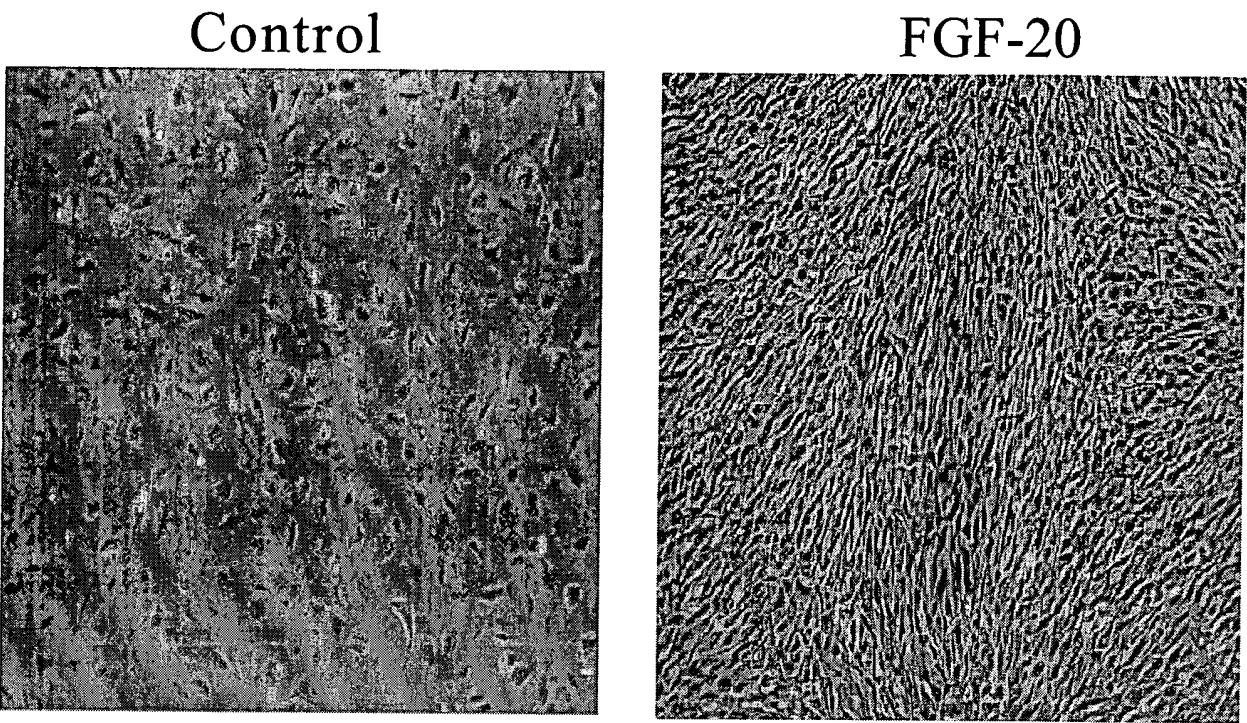


FIGURE 19.

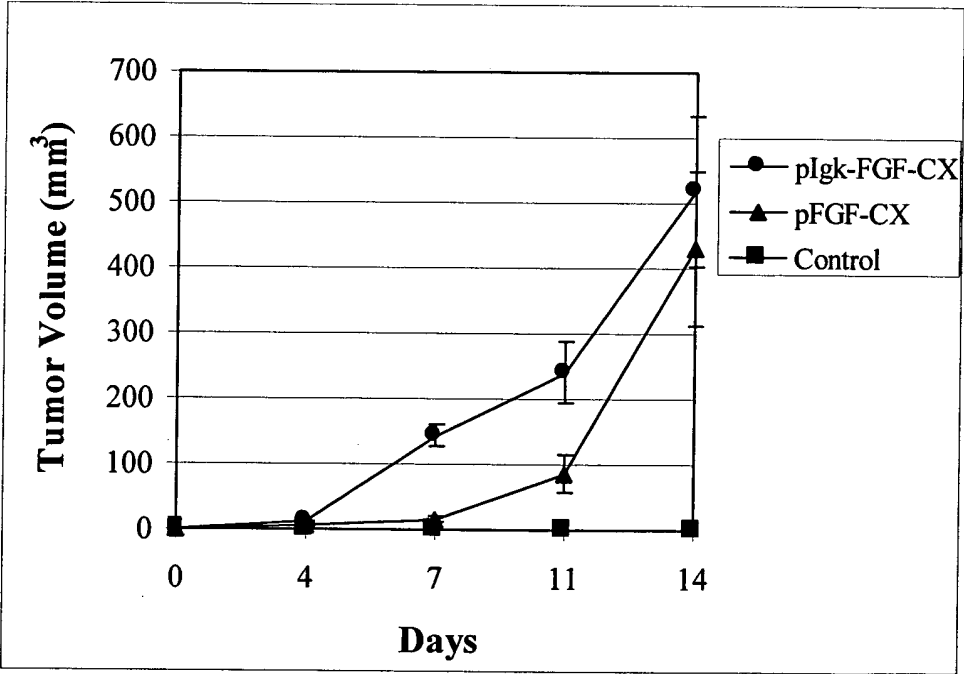
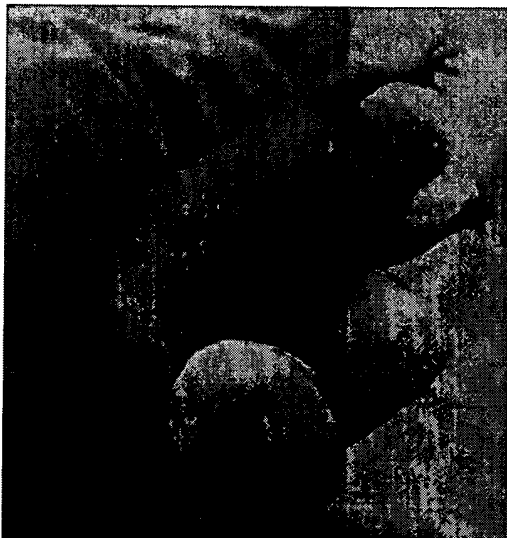


FIGURE 20.

Control



CG-AB020858



FIGURE 21.

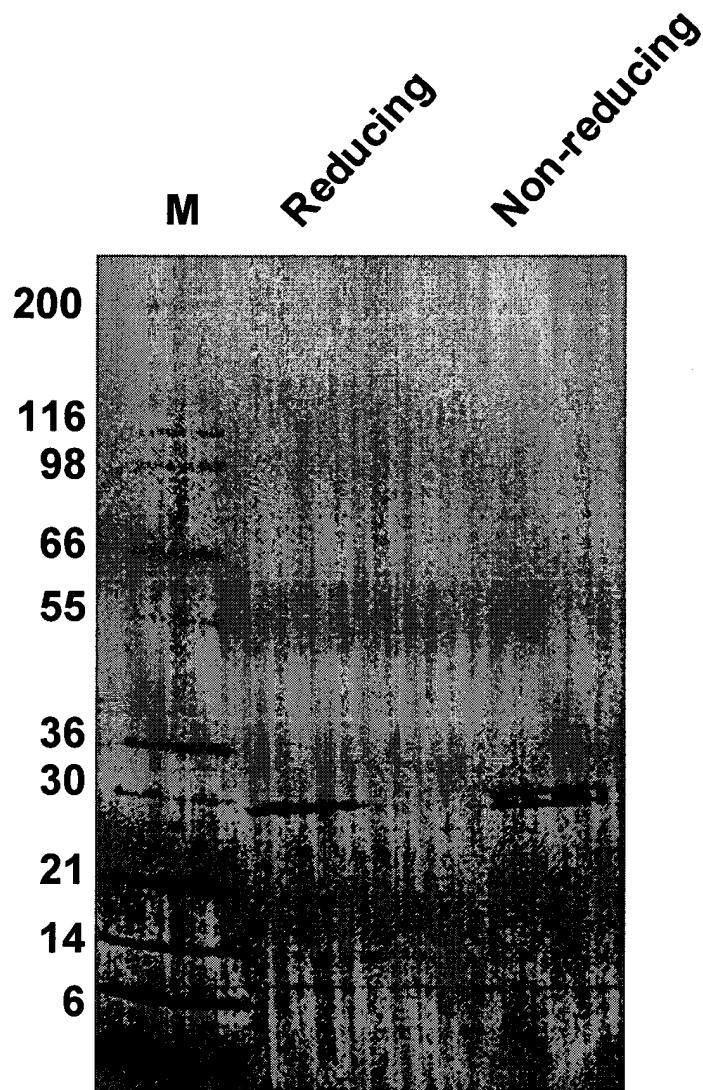


FIGURE 22.

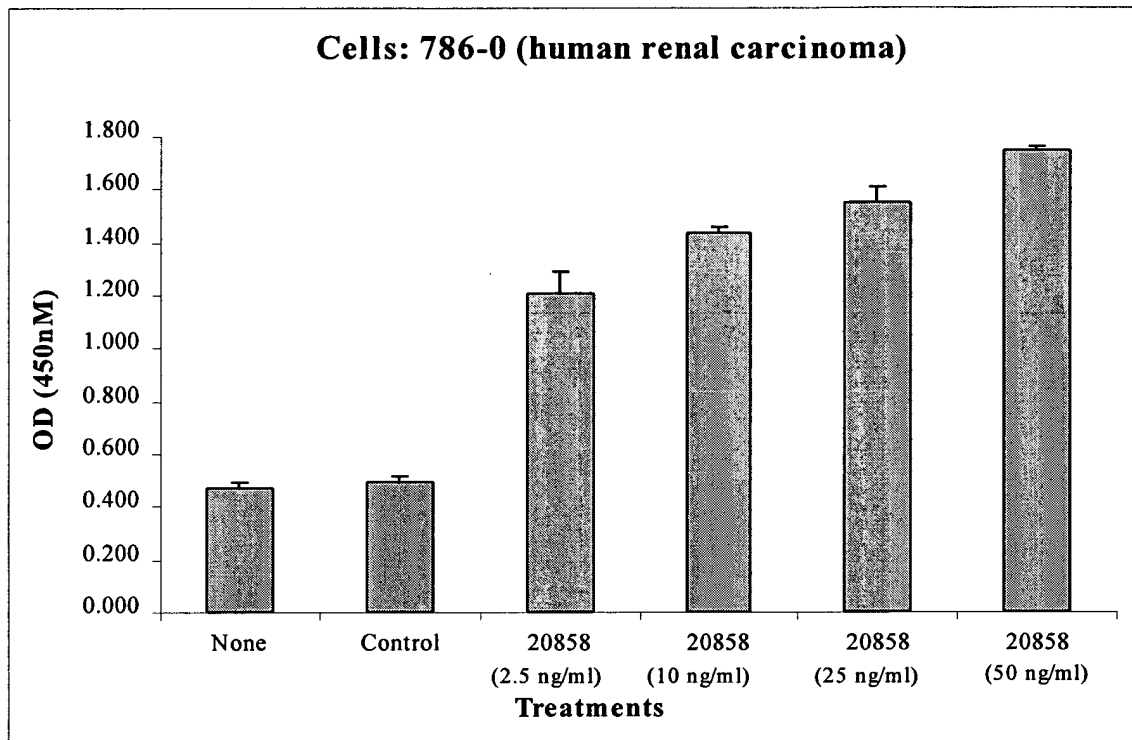
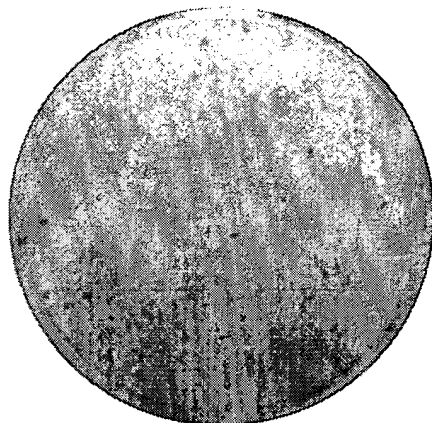
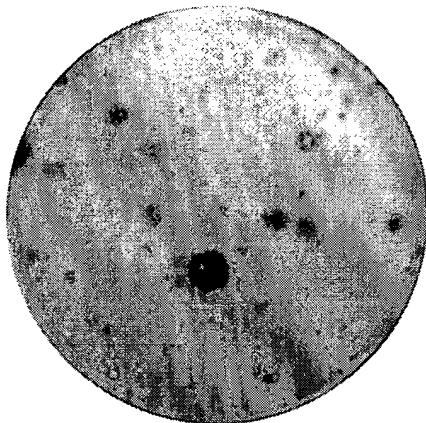


FIGURE 23.

Control



pFGF-20



pIgκ-FGF-20

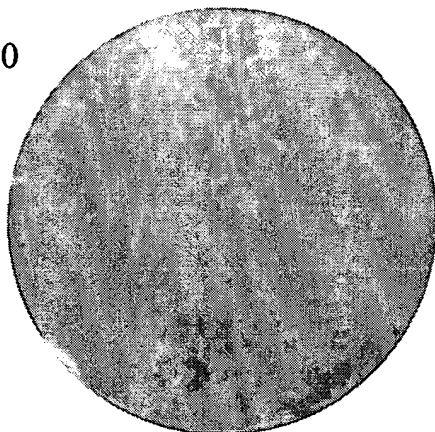


FIGURE 24

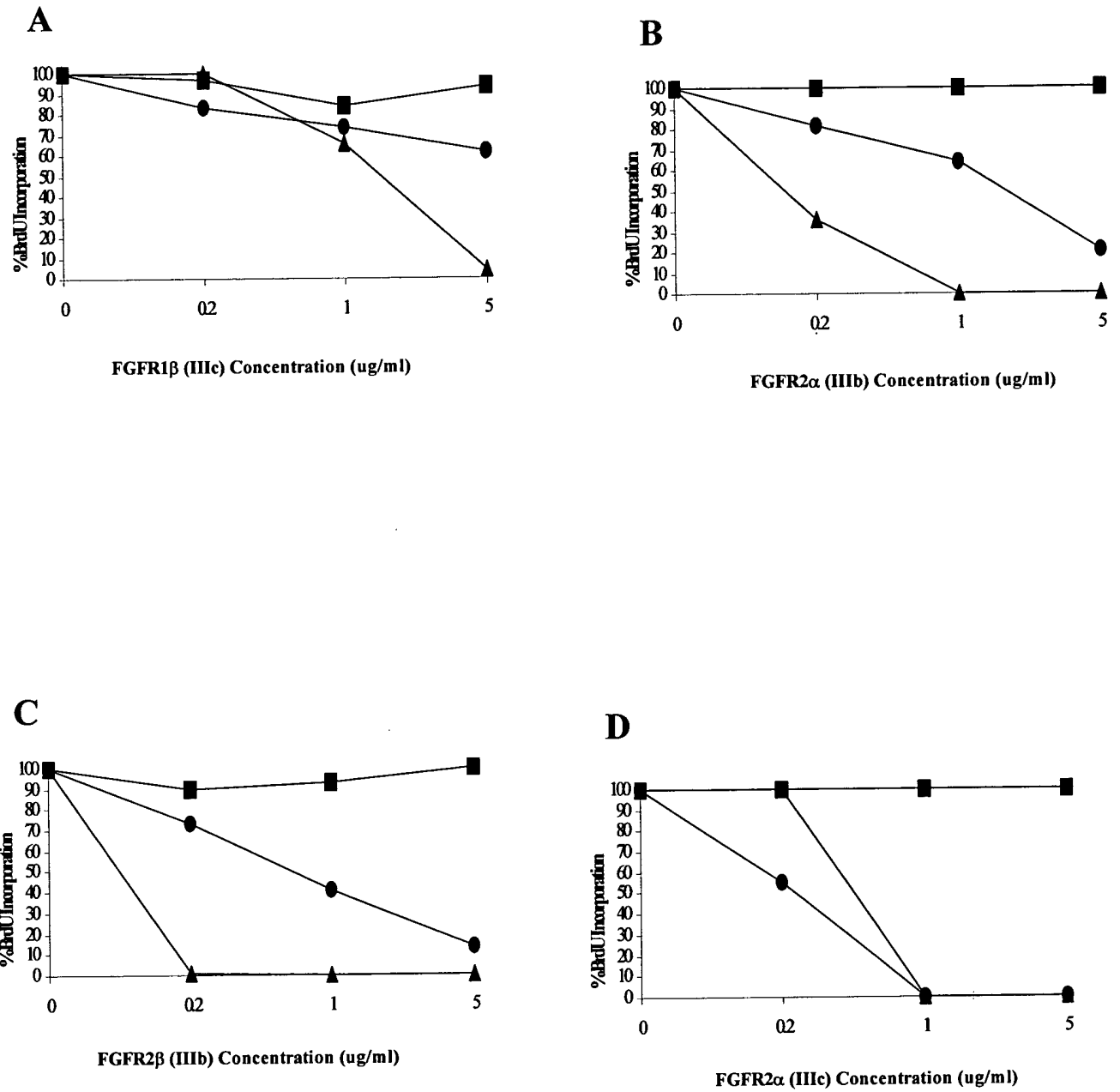


FIGURE 24 (ctd)

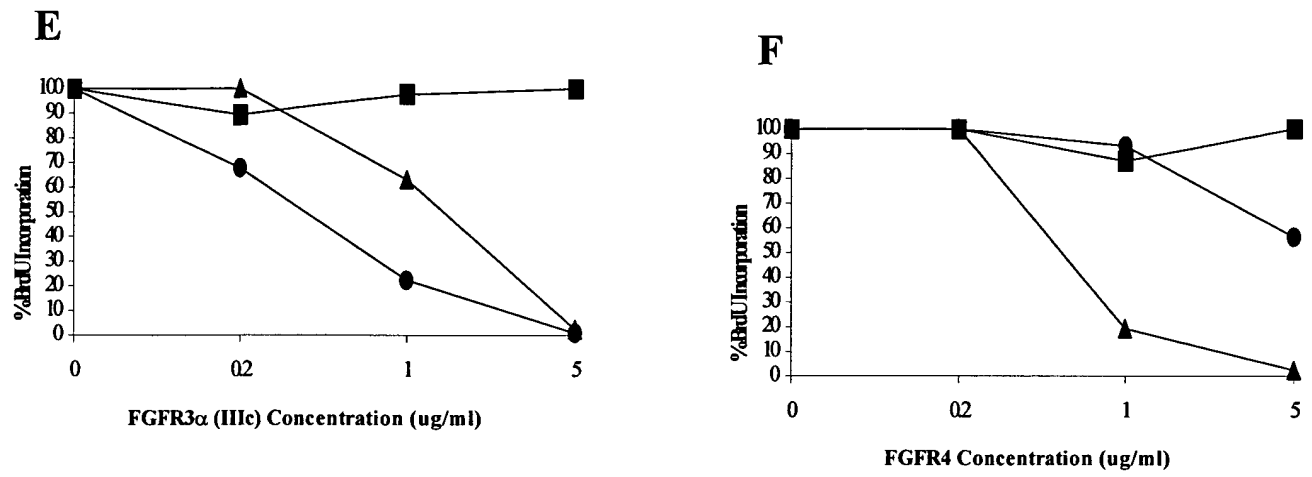


FIGURE 25

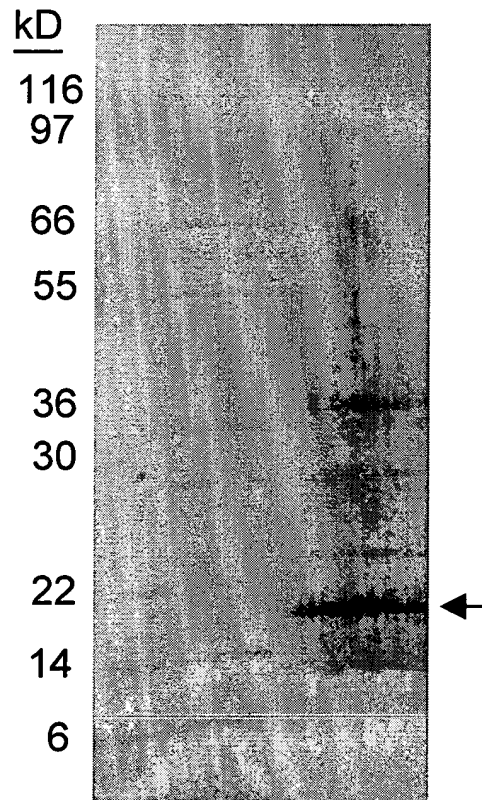


FIGURE 26

